



| Sequences producing significant alignments:                    | Score<br>(bits) | E<br>Value |
|--|-----------------|------------|
| gi 34101278 ref NP_898888.1  hypothetical protein MGC10744 ... | 299             | 3e-80      |
| gi 34101276 ref NP_115730.2  hypothetical protein MGC10744 ... | 290             | 2e-77      |
| gi 47123437 gb AAH70231.1  Unknown (protein for MGC:88213) ... | 275             | 9e-73      |
| gi 27672842 ref XP_213332.1  similar to RIKEN cDNA 1110004B... | 255             | 5e-67      |
| gi 21539609 ref NP_080114.1  RIKEN cDNA 1110004B13 [Mus mus... | 253             | 3e-66      |
| gi 21539635 ref NP_082612.1  RIKEN cDNA 1110004B13 [Mus mus... | 215             | 9e-55      |
| gi 13751660 gb AAK38512.1  DC20 [Homo sapiens]                 | 134             | 2e-30      |
| gi 47086013 ref NP_998376.1  zgc:77926 [Danio rerio] >gi 41... | 133             | 4e-30      |
| gi 47225380 emb CAG11863.1  unnamed protein product [Tetrao... | 118             | 8e-26      |
| gi 34535000 dbj BAC87177.1  unnamed protein product [Homo s... | 57              | 3e-07      |
| gi 29347399 ref NP_810902.1  conserved hypothetical protein... | 35              | 1.6        |
| gi 32421327 ref XP_331107.1  predicted protein [Neurospora ... | 35              | 1.6        |
| gi 40739337 gb EAA58527.1  hypothetical protein AN6709.2 [A... | 35              | 2.1        |
| gi 15965618 ref NP_385971.1  HYPOTHETICAL TRANSMEMBRANE PRO... | 34              | 3.9        |
| gi 13161475 emb CAC32898.1  cytochrome oxidase I [Aleochara... | 33              | 5.2        |
| gi 21402628 ref NP_658613.1  hypothetical protein predicted... | 33              | 5.2        |
| gi 47564995 ref ZP_00236038.1  membrane protein, putative [... | 33              | 5.2        |
| gi 22298906 ref NP_682153.1  molybdenum cofactor biosynthes... | 33              | 5.2        |
| gi 30022660 ref NP_834291.1  Integral membrane protein [Bac... | 33              | 5.2        |
| gi 18389591 dbj BAB84303.1  NorB homologue [Roseobacter den... | 32              | 12         |

|                                 |   |    |    |   |
|---------------------------------|---|----|----|---|
| gi 31980760 ref NP_082619.2     | RIKEN cDNA 2810439K08 [Mus mus...]      | 32 | 12 | L |
| gi 12850533 dbj BAB28760.1      | unnamed protein product [Mus mu...]     | 32 | 12 | L |
| gi 11465549 ref NP_045059.1     | unknown [Cyanidium caldarium] ...       | 32 | 12 | L |
| gi 26324794 dbj BAC26151.1      | unnamed protein product [Mus mu...]     | 32 | 12 | L |
| gi 32398820 emb CAD98530.1      | DNA topoisomerase III beta-1, p...      | 32 | 12 | L |
| gi 26327641 dbj BAC27564.1      | unnamed protein product [Mus mu...]     | 32 | 12 | L |
| gi 26338636 dbj BAC32989.1      | unnamed protein product [Mus mu...]     | 32 | 12 | L |
| gi 34857825 ref XP_218880.2     | similar to CG11737-PA [Rattus ...]      | 32 | 12 | L |
| gi 45199242 ref NP_986271.1     | AFR723Cp [Eremotheicum gossypi...]      | 32 | 17 | L |
| gi 20148896 gb AAM12701.1       | cytochrome oxidase subunit I [Co...]    | 32 | 17 | L |
| gi 23346515 ref NP_694731.1     | suppression of tumorigenicity ...       | 32 | 17 | L |
| gi 6912318 ref NP_036264.1      | claudin 8; human CLDN8 gene for...      | 32 | 17 | L |
| gi 34859740 ref XP_215667.2     | similar to Tumorsuppressor St7...       | 32 | 17 | L |
| gi 34904472 ref NP_913583.1     | OSJNBa0086P08.15 [Oryza sativa...]      | 32 | 17 | L |
| gi 32398745 emb CAD98705.1      | hypothetical predicted protein,...      | 32 | 17 | L |
| gi 20148882 gb AAM12694.1       | cytochrome oxidase subunit I [Co...]    | 31 | 22 | L |
| gi 39581918 emb CAE72880.1      | Hypothetical protein CBG20192 [...]     | 31 | 22 | L |
| gi 17553936 ref NP_497809.1     | heavy chain, Unconventional My...       | 31 | 22 | L |
| gi 48731822 ref ZP_00265566.1   | COG2375: Siderophore-interac...         | 31 | 22 | L |
| gi 15805226 ref NP_293914.1     | conserved hypothetical protein...       | 31 | 22 | L |
| gi 6679134 ref NP_032763.1      | neuropilin; Neuropilin-1 [Mus m...]     | 31 | 22 | L |
| gi 2407643 gb AAC53345.1        | neuropilin [Rattus norvegicus]          | 31 | 22 | L |
| gi 20148886 gb AAM12696.1       | cytochrome oxidase subunit I [Co...]    | 31 | 22 | L |
| gi 37805305 gb AAH60129.1       | Neuropilin [Mus musculus]               | 31 | 22 | L |
| gi 48123803 ref XP_393257.1     | similar to ENSANGP00000020727 ...       | 31 | 22 | L |
| gi 26023947 ref NP_659566.1     | neuropilin [Rattus norvegicus]...       | 31 | 22 | L |
| gi 42783762 ref NP_981009.1     | membrane protein, putative [Ba...]      | 31 | 30 | L |
| gi 13162192 emb CAC33080.1      | cytochrome oxidase I [Aleochara...]     | 31 | 30 | L |
| gi 32564324 ref NP_499385.2     | membrane Calcium ATPase, Sarco...       | 31 | 30 | L |
| gi 16081573 ref NP_393930.1     | sugar transport protein relate...       | 31 | 30 | L |
| gi 32698592 ref NP_872507.1     | p74 [Adoxophyes orana granulov...]      | 31 | 30 | L |
| gi 46111503 ref XP_382809.1     | hypothetical protein FG02633.1...       | 31 | 30 | L |
| gi 16126505 ref NP_421069.1     | phosphorylase family protein [...]      | 31 | 30 | L |
| gi 29135128 ref NP_803758.1     | ORF192 [Pseudomonas phage phiK...]      | 31 | 30 | L |
| gi 39591819 emb CAE71397.1      | Hypothetical protein CBG18305 [...]     | 31 | 30 | L |
| gi 18478322 gb AAL73125.1       | neutral endopeptidase-like prote...     | 30 | 40 | L |
| gi 2133376 pir IS58192          | hypothetical protein - Leishmania me... | 30 | 40 | L |
| gi 6118323 gb AAF04069.1        | cytochrome oxidase I [Xylosandrus...]   | 30 | 40 | L |
| gi 24762656 ref NP_611923.1     | CG13582-PA [Drosophila melanog...]      | 30 | 40 | L |
| gi 40254452 ref NP_003864.2     | neuropilin 1 [Homo sapiens] >g...       | 30 | 40 | L |
| gi 9297107 sp O14786 NRP1_HUMAN | Neuropilin-1 precursor (Vas...)         | 30 | 40 | L |
| gi 11934946 gb AAG41896.1       | neuropilin-1 [Homo sapiens]             | 30 | 40 | L |
| gi 32414281 ref XP_327620.1     | hypothetical protein [Neurospo...]      | 30 | 40 | L |
| gi 15021676 gb AAK77867.1       | neuropilin-1 [Ovis aries]               | 30 | 40 | L |
| gi 6118331 gb AAF04077.1        | cytochrome oxidase I [Xylosandrus...]   | 30 | 40 | L |
| gi 31324910 ref NP_852164.1     | cytochrome c oxidase subunit I...       | 30 | 40 | L |
| gi 2407641 gb AAC51759.1        | neuropilin [Homo sapiens]               | 30 | 40 | L |
| gi 23098373 ref NP_691839.1     | hypothetical protein OB0918 [O...       | 30 | 54 | L |
| gi 41146565 ref XP_371664.1     | KIAA1257 protein [Homo sapiens]         | 30 | 54 | L |
| gi 24270835 gb AAH38736.1       | Unknown (protein for IMAGE:52679...     | 30 | 54 | L |
| gi 21740283 emb CAD39151.1      | hypothetical protein [Homo sapi...      | 30 | 54 | L |
| gi 15615500 ref NP_243804.1     | BH2938~unknown conserved prote...       | 30 | 54 | L |

|  |    |    |   |
|--|----|----|---|
| gi 6118322 gb AAF04068.1  cytochrome oxidase I [Xyleborinus... | 30 | 54 |   |
| gi 31377711 ref NP_075069.2  hypothetical protein FLJ22104 ... | 30 | 54 | L |
| gi 21594958 gb AAH31632.1  KIAA1257 protein [Homo sapiens]     | 30 | 54 | L |
| gi 27375449 ref NP_766978.1  Alpha-methylacyl-CoA racemase ... | 30 | 54 | L |
| gi 6330918 dbj BAA86571.1  KIAA1257 protein [Homo sapiens]     | 30 | 54 |   |
| gi 19704318 ref NP_603880.1  Hypothetical protein [Fusobact... | 30 | 54 |   |
| gi 17987441 ref NP_540075.1  NADH-QUINONE OXIDOREDUCTASE CH... | 29 | 73 |   |
| gi 7519161 pir  H71023 hypothetical protein PH1485 - Pyroco... | 29 | 73 |   |
| gi 48783379 ref ZP_00279831.1  COG0477: Permeases of the ma... | 29 | 73 |   |
| gi 15896540 ref NP_349889.1  Probable cation efflux pump (m... | 29 | 73 |   |
| gi 23501689 ref NP_697816.1  NADH dehydrogenase I, A subuni... | 29 | 73 |   |
| gi 16588684 gb AAL26868.1  anion transporter/exchanger-8 [H... | 29 | 73 | L |
| gi 48825325 ref ZP_00286583.1  COG3711: Transcriptional ant... | 29 | 73 |   |
| gi 15601302 ref NP_232933.1  conserved hypothetical protein... | 29 | 73 |   |
| gi 7322060 gb AAA31968.2  ATPase subunit 6 [Naegleria fowleri] | 29 | 73 |   |
| gi 47605712 sp Q8MIB6 EFC1 PANTR ERV-F(c)1 provirus ancestr... | 29 | 73 |   |
| gi 16418457 ref NP_443193.1  solute carrier family 26, memb... | 29 | 73 | L |
| gi 19263998 gb AAH25408.1  Solute carrier family 26, member... | 29 | 73 | L |
| gi 23098187 ref NP_691653.1  hypothetical protein OB0732 [O... | 29 | 73 |   |
| gi 15810667 gb AAL08583.1  FGF2-associated protein GAFAl [H... | 29 | 73 |   |
| gi 9453728 emb CAB99354.1  bA48209.4 (Novel sulphate transp... | 29 | 73 | L |
| gi 47219823 emb CAG03450.1  unnamed protein product [Tetrao... | 29 | 73 |   |
| gi 20336285 ref NP_619732.1  solute carrier family 26, memb... | 29 | 73 | L |
| gi 40742890 gb EAA62080.1  hypothetical protein AN7500.2 [A... | 29 | 73 |   |
| gi 41724135 ref ZP_00151001.1  COG1742: Uncharacterized con... | 29 | 73 |   |
| gi 6562165 emb CAB62533.1  hypothetical protein [Homo sapiens] | 29 | 73 | L |
| gi 37546246 ref XP_066621.3  similar to envelope protein [H... | 29 | 73 | L |
| gi 46435250 gb EAK94636.1  hypothetical protein Ca019.11163... | 29 | 73 |   |

### Alignments

Get selected sequences  Select all  Deselect all

>gi|34101278|ref|NP\_898888.1| L hypothetical protein MGC10744 isoform 2 [Homo sa  
gi|37182173|gb|AAQ88889.1| GRVS638 [Homo sapiens]  
Length = 140

Score = 299 bits (699), Expect = 3e-80  
Identities = 114/141 (80%), Positives = 118/141 (83%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPSRFLTLTAHLN--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54  
MGRVSGLVPSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDIQLV SV

Sbjct: 1 MGRVSGLVPSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSV 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISIGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107  
TLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTYWYI+ FCS

Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQLSISIGAHCSASVALSFFIFERWECTTYWYIFVFCSA 119

Query: 108 MPAVTEMATW-TVFGLKKKPF 127  
+PAVTEMA + TVFGLKKKPF

Sbjct: 120 LPAPVTEMALFVTVFGLKKKPF 140

>gi|34101276|ref|NP\_115730.2| **L** hypothetical protein MGC10744 isoform 1 [Homo sa  
Length = 146

Score = 290 bits (677), Expect = 2e-77  
Identities = 113/147 (76%), Positives = 117/147 (79%), Gaps = 21/147 (14%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50  
MGRVSGLVPNSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDI L  
Sbjct: 1 MGRVSGLVPNSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYI 103  
V SVTLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTYWYI  
Sbjct: 60 VAALSVTGLFAVELAGFLSGVSMFNSTQSLISIGAHCASASVALSFFIFERWECTTYWYI 119

Query: 104 W-FCS-MPAVTEMATW-TVFGLKKPF 127  
+ FCS +PAVTEMA + TVFGLKKPF  
Sbjct: 120 FVFCALPAVTEMALFVTVFGLKKPF 146

>gi|47123437|gb|AAH70231.1| Unknown (protein for MGC:88213) [Homo sapiens]  
Length = 139

Score = 275 bits (641), Expect = 9e-73  
Identities = 108/145 (74%), Positives = 112/145 (77%), Gaps = 24/145 (16%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50  
MGRVSGLVPNSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDI L  
Sbjct: 1 MGRVSGLVPNSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYI 103  
V SVTLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTY  
Sbjct: 60 VAALSVTGLFAVELAGFLSGVSMFNSTQSLISIGAHCASASVALSFFIFERWECTTY-- 116

Query: 104 WFCMSMPAVTEMATW-TVFGLKKPF 127  
C+PAVTEMA + TVFGLKKPF  
Sbjct: 117 --CALPAVTEMALFVTVFGLKKPF 139

>gi|27672842|ref|XP\_213332.1| **L** similar to RIKEN cDNA 1110004B13 [Rattus norvegi  
Length = 140

Score = 255 bits (596), Expect = 5e-67  
Identities = 103/141 (73%), Positives = 111/141 (78%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--TLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54  
MGR+SGLVPSRFLTL AHL I TL SR+SNIQACLPL FTPEEY+KQD QLV +  
Sbjct: 1 MGRISGLVPSRFLTLAHLVIVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107  
TLGLFA GFLSGVSM STQL+SI CSASV +SFFIFERWECTTYWYI+ FCS  
Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQSLISIAAHCSASVALSFFIFERWECTTYWYIFAFCSA 119

Query: 108 MPAVTEMATW-TVFGLKKPF 127  
PAVTE A + VFGLKKPF  
Sbjct: 120 FPAVTETALFIAVFGLKKPF 140

□ >gi|21539609|ref|NP\_080114.1| L RIKEN cDNA 1110004B13 [Mus musculus]  
 gi|12834053|dbj|BAB22768.1| L unnamed protein product [Mus musculus]  
 Length = 140

Score = 253 bits (590), Expect = 3e-66  
 Identities = 102/141 (72%), Positives = 111/141 (78%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54  
 MGR+SGLVPSRFLTL AHL ITL SR+SNIQACLPL FTPEEY+KQD QLV +  
 Sbjct: 1 MGRISGLVPSRFLTLAAHVVVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISIGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107  
 TLGLFA GFLSGVSM STQLS+SI CSASV +SFF+FERWECTTYWYI+ FCS  
 Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQSLISIAAHCSASVALSFFVFERWECTTYWYIIFTFC 119

Query: 108 MPAVTEMATW-TVFGLKKKPF 127  
 PAVTE A + VFGLKKKPF  
 Sbjct: 120 FPAVTETALFIAVFGLKKKPF 140

□ >gi|21539635|ref|NP\_082612.1| L RIKEN cDNA 1110004B13 [Mus musculus]  
 gi|12850002|dbj|BAB28560.1| L unnamed protein product [Mus musculus]  
 Length = 143

Score = 215 bits (500), Expect = 9e-55  
 Identities = 85/118 (72%), Positives = 93/118 (78%), Gaps = 13/118 (11%)

Query: 1 MGRVSGLVPSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54  
 MGR+SGLVPSRFLTL AHL ITL SR+SNIQACLPL FTPEEY+KQD QLV +  
 Sbjct: 1 MGRISGLVPSRFLTLAAHVVVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISIGM-CSASV-MSFFIFERWECTTYWYIW-FC 106  
 TLGLFA GFLS VSM STQLS+SI CSASV +SFF+FERWECTTYWYI+ FC  
 Sbjct: 60 TLGLFAVELAGFLSRVSMFNSTQSLISIAAHCSASVALSFFVFERWECTTYWYIIFTFC 117

□ >gi|13751660|gb|AAK38512.1| L DC20 [Homo sapiens]  
 Length = 141

Score = 134 bits (309), Expect = 2e-30  
 Identities = 52/69 (75%), Positives = 52/69 (75%), Gaps = 13/69 (18%)

Query: 1 MGRVSGLVPSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50  
 MGRVSGLVPSRFLTL AHL ITL SRDSNIQACLPLFTPEEYDKQDI L  
 Sbjct: 1 MGRVSGLVPSRFLTLAAHVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLG 57  
 V SVTLG  
 Sbjct: 60 VAALSVTLG 68

□ >gi|47086013|ref|NP\_998376.1| L zgc:77926 [Danio rerio]  
 gi|41351480|gb|AAH65897.1| L Zgc:77926 [Danio rerio]

Length = 135

Score = 133 bits (307), Expect = 4e-30  
 Identities = 68/123 (55%), Positives = 83/123 (67%), Gaps = 18/123 (14%)

Query: 7 LVPSRFLTLTAHLNITLD---SRDSNIQACLPLTFTPEEYDKQDIQL--VWSVTLGLF-- 59  
 LVP+RFLTLTAHL I + SRD+NIQ+CLPL FT +Y +D +L SVTL LF

Sbjct: 7 LVPARFLTLTAHLVIIITIFWSRDNNIQSCLPLEFTEDQYRTEDTRLTVALSVTLALFVL 66

Query: 60 --AWMGFLSGVSM-MTQSLIS-IGMCSASV-MSFFIFERWECTTYWYIWF--CSM-PAV 111  
 A GFLSGVSM S Q+L+S I SA V +SFF+F +W C TYW I F CS+ PAV

Sbjct: 67 ELA--GFLSGVSMFNSNQALLSLITHSSACVCLSFFVHQWPCWTYWII-FSICSVFPAV 123

Query: 112 TEM 114

E+

Sbjct: 124 VEL 126

>gi|47225380|emb|CAG11863.1| unnamed protein product [Tetraodon nigroviridis]

Length = 180

Score = 118 bits (273), Expect = 8e-26  
 Identities = 58/110 (52%), Positives = 78/110 (70%), Gaps = 10/110 (9%)

Query: 4 VSGLVPSRFLTLTAHLNITLD---SRDSNIQACLPLTFTPEEYDKQDIQLV--WSVTLGL 58  
 VS LVP+RFLT+ AHL I + SR++N++A LPL FT E+YD +D +LV +VT+G+

Sbjct: 4 VSSLVPARFLTIIAHLVIVITIFWSRENNVRAGLPLDFTQEYDSEDRKLVIALAVTIGM 63

Query: 59 FA--WMGFLSGVSMMS-TQSLISIGM-CSASV-MSFFIFERWECTTYWYI 103

FA GF SGVSM + +Q L+S G SASV + FF+FE+WEC YW+I

Sbjct: 64 FAIELAGFFSGVSMFNCQGLLSTGTHASASVALLFFLFEQWECDIYWWI 113

>gi|34535000|dbj|BAC87177.1| unnamed protein product [Homo sapiens]

Length = 163

Score = 57.5 bits (128), Expect = 3e-07  
 Identities = 21/25 (84%), Positives = 21/25 (84%), Gaps = 2/25 (8%)

Query: 1 MGRVSGLVPSRFLTLTAHL--NITL 23

MGRVSGLVPSRFLTL AHL ITL

Sbjct: 1 MGRVSGLVPSRFLTLAHLVVVITL 25

>gi|29347399|ref|NP\_810902.1| conserved hypothetical protein [Bacteroides thetai VPI-5482]

gi|29339299|gb|AAO77096.1| conserved hypothetical protein [Bacteroides thetaiotaao VPI-5482]

Length = 360

Score = 35.0 bits (75), Expect = 1.6

Identities = 17/42 (40%), Positives = 21/42 (50%), Gaps = 21/42 (50%)

Query: 36 LTFTPEEYDKQDIQLVWSVTLGL-----FAWMG 63

LTFT EYD++DI+ LGL FA+MG

Sbjct: 198 LTFT-EEYDERDIE-----LGLIKHIEKFLVEMGAGFAFMG 232

□ >gi|32421327|ref|XP\_331107.1| predicted protein [Neurospora crassa]  
gi|28921209|gb|EAA30521.1| predicted protein [Neurospora crassa]  
Length = 155

Score = 35.0 bits (75), Expect = 1.6  
Identities = 10/13 (76%), Positives = 10/13 (76%), Gaps = 2/13 (15%)

Query: 108 MPAVTEMATWTVF 120  
MP TEM TWTVF  
Sbjct: 130 MP--TEMPTWTVF 140

□ >gi|40739337|gb|EAA58527.1| hypothetical protein AN6709.2 [Aspergillus nidulans]  
Length = 1999

Score = 34.6 bits (74), Expect = 2.1  
Identities = 13/24 (54%), Positives = 17/24 (70%), Gaps = 2/24 (8%)

Query: 61 WMGFLSGVS--MMSTQSLISIGMC 82  
WM FLSG+S M TQ+L +I +C  
Sbjct: 1075 WMSFLSGLSAPMQDTQNLKTIKLC 1098

□ >gi|15965618|ref|NP\_385971.1| HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium  
gi|15074799|emb|CAC46444.1| HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium mel  
Length = 302

Score = 33.7 bits (72), Expect = 3.9  
Identities = 14/26 (53%), Positives = 17/26 (65%), Gaps = 9/26 (34%)

Query: 50 LVWSVTLGL--FA-----WMGFLSGV 68  
L+WSVTLG+ FA WM L+GV  
Sbjct: 247 LLWSVTLGVVFFAETPDRWM--LAGV 270

□ >gi|13161475|emb|CAC32898.1| cytochrome oxidase I [Aleochara cf. chrysorrhoea]  
Length = 457

Score = 33.3 bits (71), Expect = 5.2  
Identities = 16/31 (51%), Positives = 16/31 (51%), Gaps = 11/31 (35%)

Query: 68 VSMMSTQSLISIGMCSASVMS--FFIFERWE 96  
VS M SLIS M MS FFIF WE  
Sbjct: 397 VSSMG--SLIS--M-----MSIIFFIFIWE 418

□ >gi|21402628|ref|NP\_658613.1| hypothetical protein predicted by GeneMark [Bacillus  
A2012]  
gi|30264655|ref|NP\_847032.1| membrane protein, putative [Bacillus anthracis str.  
gi|47530125|ref|YP\_021474.1| membrane protein, putative [Bacillus anthracis str.  
gi|30259330|gb|AAP28518.1| membrane protein, putative [Bacillus anthracis str. Am

gi|47505273|gb|AAT33949.1| membrane protein, putative [Bacillus anthracis str. Am  
Length = 210

Score = 33.3 bits (71), Expect = 5.2  
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87  
S+I IGMCSA+VM  
Sbjct: 36 SIIIIGMCSAAVM 48

gi|47564995|ref|ZP\_00236038.1| membrane protein, putative [Bacillus cereus G924  
gi|47557781|gb|EAL16106.1| membrane protein, putative [Bacillus cereus G9241]  
Length = 210

Score = 33.3 bits (71), Expect = 5.2  
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87  
S+I IGMCSA+VM  
Sbjct: 36 SIIIIGMCSAAVM 48

gi|22298906|ref|NP\_682153.1| molybdenum cofactor biosynthesis protein A [Thermo  
elongatus BP-1]  
gi|22295087|dbj|BAC08915.1| molybdenum cofactor biosynthesis protein A [Thermosyn  
elongatus BP-1]  
Length = 332

Score = 33.3 bits (71), Expect = 5.2  
Identities = 18/37 (48%), Positives = 19/37 (51%), Gaps = 14/37 (37%)

Query: 7 LVPSRFLTLTAH----LNITLDSRDSNIQACLPLTF 38  
LVP FL L AH LNI+LDS D P TF  
Sbjct: 120 LVP--FLPLLAHYGVRRLNISLDSL-----PQTF 147

gi|30022660|ref|NP\_834291.1| Integral membrane protein [Bacillus cereus ATCC 14  
gi|29898218|gb|AAP11492.1| Integral membrane protein [Bacillus cereus ATCC 14579]  
Length = 210

Score = 33.3 bits (71), Expect = 5.2  
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87  
S+I IGMCSA+VM  
Sbjct: 36 SIIIIGMCSAAVM 48

gi|18389591|dbj|BAB84303.1| NorB homologue [Roseobacter denitrificans]  
Length = 434

Score = 32.0 bits (68), Expect = 12  
Identities = 21/56 (37%), Positives = 25/56 (44%), Gaps = 21/56 (37%)

Query: 43 YDKQDIQLV-WSVTLGLFA-----WM----GFLSG-----VSMMSTQSLI 77  
 Y Q I LV ++V LGLFA W+ FLS V M+ T SLI  
 Sbjct: 3 YQSQSIALVYFAVALGLFAIQVSGGLLGWIYVSPNFLSEILPFNIVRMLHTNSLI 58

>gi|31980760|ref|NP\_082619.2| L RIKEN cDNA 2810439K08 [Mus musculus]  
 gi|26324358|dbj|BAC25933.1| L unnamed protein product [Mus musculus]  
 Length = 458

Score = 32.0 bits (68), Expect = 12  
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSMM---STQSLISIGM 81  
 GFL+GVSMM ST +I M  
 Sbjct: 334 GFLAGVSMMFYKST---TISM 351

>gi|12850533|dbj|BAB28760.1| L unnamed protein product [Mus musculus]  
 gi|15192728|gb|AAK84685.1| L putative transmembrane protein [Mus musculus]  
 gi|23273857|gb|AAH33279.1| L RIKEN cDNA 2810439K08 [Mus musculus]  
 gi|29748020|gb|AAH50931.1| L RIKEN cDNA 2810439K08 [Mus musculus]  
 Length = 458

Score = 32.0 bits (68), Expect = 12  
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSMM---STQSLISIGM 81  
 GFL+GVSMM ST +I M  
 Sbjct: 334 GFLAGVSMMFYKST---TISM 351

>gi|11465549|ref|NP\_045059.1| unknown [Cyanidium caldarium]  
 gi|6136624|sp|O19887|YC53\_CYACA Hypothetical 28.1 kDa protein ycf53  
 gi|7484284|pir||T11955 hypothetical protein ORF237 - red alga (Cyanidium caldarium)  
 chloroplast  
 gi|2465773|gb|AAB82702.1| unknown [Cyanidium caldarium]  
 Length = 237

Score = 32.0 bits (68), Expect = 12  
 Identities = 15/31 (48%), Positives = 18/31 (58%), Gaps = 10/31 (32%)

Query: 1 MGRVSGLVPSRFLTLTAHLNITLDSRDSNIQ 31  
 M R+ RF++L LN LDS DSNIQ  
 Sbjct: 1 MNRI-----RFISLI--LN--LDSCDSNIQ 21

>gi|26324794|dbj|BAC26151.1| L unnamed protein product [Mus musculus]  
 Length = 458

Score = 32.0 bits (68), Expect = 12  
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSMM---STQSLISIGM 81